

#7

TECH CENTER 1600/2900

NOV 13 2001

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/848,035

DATE: 09/21/2001

TIME: 18:04:35

Input Set : A:\SEQUENCE LISTING.TXT

Output Set: N:\CRF3\09212001\I848035.raw

4 <110> APPLICANT: Bertin, John

6 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE NBS/LRR PROTEIN FAMILY AND USES
THEREOF

8 <130> FILE REFERENCE: 07334-268001

10 <140> CURRENT APPLICATION NUMBER: US 09/848,035

11 <141> CURRENT FILING DATE: 2001-05-03

13 <150> PRIOR APPLICATION NUMBER: US 60/201,464

14 <151> PRIOR FILING DATE: 2000-05-03

16 <160> NUMBER OF SEQ ID NOS: 17

18 <170> SOFTWARE: FastSEQ for Windows Version 4.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 2464

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (1)...(2463)

29 <400> SEQUENCE: 1

30	atg	aca	tcg	ccc	cag	cta	gag	tgg	act	ctg	cag	acc	ctt	ctg	gag	cag	48
31	Met	Thr	Ser	Pro	Gln	Leu	Glu	Trp	Thr	Leu	Gln	Thr	Leu	Leu	Glu	Gln	
32	1				5				10					15			
34	ctg	aac	gag	gat	gaa	tta	aag	agt	ttc	aaa	tcc	ctt	tta	tgg	gct	ttt	96
35	Leu	Asn	Glu	Asp	Glu	Leu	Lys	Ser	Phe	Lys	Ser	Leu	Leu	Trp	Ala	Phe	
36				20				25				30					
38	ccc	ctc	gaa	gac	gtg	cta	cag	aag	acc	cca	tgg	tct	gag	gtg	gaa	gag	144
39	Pro	Leu	Glu	Asp	Val	Leu	Gln	Lys	Thr	Pro	Trp	Ser	Glu	Val	Glu	Glu	
40			35				40				45						
42	gct	gat	ggc	aag	aaa	ctg	gca	gaa	att	ctg	gtc	aac	acc	tcc	tca	gaa	192
43	Ala	Asp	Gly	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Val	Asn	Thr	Ser	Ser	Glu	
44		50				55			60								
46	aat	tgg	ata	agg	aat	gcg	act	gtg	aac	atc	ttg	gaa	gag	atg	aat	ctc	240
47	Asn	Trp	Ile	Arg	Asn	Ala	Thr	Val	Asn	Ile	Leu	Glu	Glu	Met	Asn	Leu	
48	65				70				75					80			
50	acg	gaa	ttg	tgt	aag	atg	gca	aag	gct	gag	atg	atg	gag	gac	gga	cag	288
51	Thr	Glu	Leu	Cys	Lys	Met	Ala	Lys	Ala	Glu	Met	Met	Glu	Asp	Gly	Gln	
52				85					90					95			
54	gtg	caa	gaa	ata	gat	aat	cct	gag	ctg	gga	gat	gca	gaa	gaa	gac	tcg	336
55	Val	Gln	Glu	Ile	Asp	Asn	Pro	Glu	Leu	Gly	Asp	Ala	Glu	Glu	Asp	Ser	
56			100					105				110					
58	gag	tta	gca	aag	cca	ggt	gaa	aag	gaa	gga	tgg	aga	aat	tca	atg	gag	384
59	Glu	Leu	Ala	Lys	Pro	Gly	Glu	Lys	Glu	Gly	Trp	Arg	Asn	Ser	Met	Glu	
60			115					120				125					
62	aaa	caa	tct	ttg	gtc	tgg	aag	aac	acc	ttt	tgg	caa	gga	gac	att	gac	432
63	Lys	Gln	Ser	Leu	Val	Trp	Lys	Asn	Thr	Phe	Trp	Gln	Gly	Asp	Ile	Asp	
64		130				135			140								
66	aat	ttc	cat	gac	gac	gtc	act	ctg	aga	aac	caa	cgg	ttc	att	cca	ttc	480
67	Asn	Phe	His	Asp	Asp	Val	Thr	Leu	Arg	Asn	Gln	Arg	Phe	Ile	Pro	Phe	
68	145				150				155					160			

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70	ttg aat ccc aga aca ccc agg aag cta aca cct tac acg gtg gtg ctg	528
71	Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu	
72	165 170 175	
74	cac ggc ccc gca ggc gtg ggg aaa acc acg ctg gcc aaa aag tgt atg	576
75	His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met	
76	180 185 190	
78	ctg gac tgg aca gac tgc aac ctc agc ccg acg ctc aga tac gcg ttc	624
79	Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe	
80	195 200 205	
82	tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca	672
83	Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala	
84	210 215 220	
86	gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc	720
87	Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser	
88	225 230 235 240	
90	atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat	768
91	Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp	
92	245 250 255	
94	gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac	816
95	Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp	
96	260 265 270	
98	tgg gag aag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag	864
99	Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys	
100	275 280 285	
102	agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg ccg ccc agg	912
103	Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg	
104	290 295 300	
106	gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac ata agg	960
107	Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Pro Ile Tyr Ile Arg	
108	305 310 315 320	
110	gtg gag ggc ttc ctg gag gag gac agg agg gcc tat ttc ctg aga cac	1008
111	Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His	
112	325 330 335	
114	ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc	1056
115	Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser	
116	340 345 350	
118	aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att	1104
119	Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile	
120	355 360 365	
122	gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccg ccg	1152
123	Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro	
124	370 375 380	
126	gtt ccc gca ggg cgc aca gct gcg ggg cgc gct gcg gac gct gag cct	1200
127	Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro	
128	385 390 395 400	
130	cct ggc cgc gca ggg ctg tgg gcg cag atg tcc gtg ttc cac cga gag	1248
131	Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu	
132	405 410 415	
134	gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg	1296

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135	Asp	Leu	Glu	Arg	Leu	Gly	Val	Gln	Glu	Ser	Asp	Leu	Arg	Leu	Phe	Leu	
136				420					425					430			
138	gac	gga	gac	atc	ctc	cgc	cag	gac	aga	gtc	tcc	aaa	ggc	tgc	tac	tcc	1344
139	Asp	Gly	Asp	Ile	Leu	Arg	Gln	Asp	Arg	Val	Ser	Lys	Gly	Cys	Tyr	Ser	
140				435				440					445				
142	ttc	atc	cac	ctc	agc	ttc	cag	cag	ttt	ctc	act	gcc	ctg	ttc	tac	gcc	1392
143	Phe	Ile	His	Leu	Ser	Phe	Gln	Gln	Phe	Leu	Thr	Ala	Leu	Phe	Tyr	Ala	
144				450				455					460				
146	ctg	gag	aag	gag	gag	gag	gag	gac	agg	gac	ggc	cac	gcc	tgg	gac	att	1440
147	Leu	Glu	Lys	Glu	Glu	Glu	Glu	Asp	Arg	Asp	Gly	His	Ala	Trp	Asp	Ile	
148	465						470				475					480	
150	ggg	gac	gta	cag	aag	ctg	ctt	tcc	gga	gaa	gaa	aga	ctc	aag	aac	ccc	1488
151	Gly	Asp	Val	Gln	Lys	Leu	Leu	Ser	Gly	Glu	Glu	Arg	Leu	Lys	Asn	Pro	
152					485						490				495		
154	gac	ctg	att	caa	gta	gga	cac	ttc	tta	ttc	ggc	ctc	gct	aac	gag	aag	1536
155	Asp	Leu	Ile	Gln	Val	Gly	His	Phe	Leu	Phe	Gly	Leu	Ala	Asn	Glu	Lys	
156				500					505				510				
158	aga	gcc	aag	gag	ttg	gag	gcc	act	ttt	ggc	tgc	cgg	atg	tca	ccg	gac	1584
159	Arg	Ala	Lys	Glu	Leu	Glu	Ala	Thr	Phe	Gly	Cys	Arg	Met	Ser	Pro	Asp	
160				515				520					525				
162	atc	aaa	cag	gaa	ttg	ctg	caa	tgc	aaa	gca	cat	ctt	cat	gca	aat	aag	1632
163	Ile	Lys	Gln	Glu	Leu	Leu	Gln	Cys	Lys	Ala	His	Leu	His	Ala	Asn	Lys	
164				530				535					540				
166	ccc	tta	tcc	gtg	acc	gac	ctg	aag	gag	gtc	ttg	ggc	tgc	ctg	tat	gag	1680
167	Pro	Leu	Ser	Val	Thr	Asp	Leu	Lys	Glu	Val	Leu	Gly	Cys	Leu	Tyr	Glu	
168	545					550					555					560	
170	tct	cag	gag	gag	gag	ctg	gcg	aag	gtg	gtg	gtg	gcc	ccg	ttc	aag	gaa	1728
171	Ser	Gln	Glu	Glu	Glu	Leu	Ala	Lys	Val	Val	Val	Ala	Pro	Phe	Lys	Glu	
172					565					570					575		
174	att	tct	att	cac	ctg	aca	aat	act	tct	gaa	gtg	atg	cat	tgt	tcc	ttc	1776
175	Ile	Ser	Ile	His	Leu	Thr	Asn	Thr	Ser	Glu	Val	Met	His	Cys	Ser	Phe	
176				580					585					590			
178	agc	ctg	aag	cat	tgt	caa	gac	ttg	cag	aaa	ctc	tca	ctg	cag	gta	gca	1824
179	Ser	Leu	Lys	His	Cys	Gln	Asp	Leu	Gln	Lys	Leu	Ser	Leu	Gln	Val	Ala	
180				595				600					605				
182	aag	ggg	gtg	ttc	ctg	gag	aat	tac	atg	gat	ttt	gaa	ctg	gac	att	gaa	1872
183	Lys	Gly	Val	Phe	Leu	Glu	Asn	Tyr	Met	Asp	Phe	Glu	Leu	Asp	Ile	Glu	
184				610				615				620					
186	ttt	gaa	agc	tca	aac	agc	aac	ctc	aag	ttt	ctg	gaa	gtg	aaa	caa	agc	1920
187	Phe	Glu	Ser	Ser	Asn	Ser	Asn	Leu	Lys	Phe	Leu	Glu	Val	Lys	Gln	Ser	
188	625					630					635				640		
190	ttc	ctg	agt	gac	tct	tct	gtg	cgg	att	ctt	tgt	gac	cac	gta	acc	cgt	1968
191	Phe	Leu	Ser	Asp	Ser	Ser	Val	Arg	Ile	Leu	Cys	Asp	His	Val	Thr	Arg	
192					645					650					655		
194	agc	acc	tgt	cat	ctg	cag	aaa	gtg	gag	att	aaa	aac	gtc	acc	cct	gac	2016
195	Ser	Thr	Cys	His	Leu	Gln	Lys	Val	Glu	Ile	Lys	Asn	Val	Thr	Pro	Asp	
196				660					665					670			
198	acc	gcg	tac	cgg	gac	ttc	tgt	ctt	gct	ttc	att	ggg	aag	aag	acc	ctc	2064
199	Thr	Ala	Tyr	Arg	Asp	Phe	Cys	Leu	Ala	Phe	Ile	Gly	Lys	Lys	Thr	Leu	

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200          675          680          685
202 acg cac ctg acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg      2112
203 Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met
204          690          695          700
206 ctg atg ctg tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac      2160
207 Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr
208 705          710          715          720
210 ctg agg ttg gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc      2208
211 Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe
212          725          730          735
214 ttc tat gtc ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca      2256
215 Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser
216          740          745          750
218 gcc aat gtg ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg      2304
219 Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met
220          755          760          765
222 aca cgc cca aaa cac ttc ctg cag atg ttg tgc ttg gaa aac tgt cgt      2352
223 Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg
224          770          775          780
226 ctt aca gaa gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc      2400
227 Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser
228 785          790          795          800
230 aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca      2448
231 Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr
232          805          810          815
234 ggg gtg aag ttt ctg t      2464
235 Gly Val Lys Phe Leu
236          820
238 <210> SEQ ID NO: 2
239 <211> LENGTH: 821
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
243 <400> SEQUENCE: 2
244 Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln
245 1          5          10          15
246 Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe
247          20          25          30
248 Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu
249          35          40          45
250 Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu
251          50          55          60
252 Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu
253 65          70          75          80
254 Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln
255          85          90          95
256 Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser
257          100          105          110
258 Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu
259          115          120          125

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260 Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp
261      130      135      140
262 Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe
263 145      150      155      160
264 Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu
265      165      170      175
266 His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met
267      180      185      190
268 Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe
269      195      200      205
270 Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala
271      210      215      220
272 Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser
273 225      230      235      240
274 Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp
275      245      250      255
276 Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp
277      260      265      270
278 Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys
279      275      280      285
280 Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg
281      290      295      300
282 Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg
283 305      310      315      320
284 Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His
285      325      330      335
286 Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser
287      340      345      350
288 Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile
289      355      360      365
290 Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro
291      370      375      380
292 Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro
293 385      390      395      400
294 Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu
295      405      410      415
296 Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu
297      420      425      430
298 Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser
299      435      440      445
300 Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala
301      450      455      460
302 Leu Glu Lys Glu Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile
303 465      470      475      480
304 Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro
305      485      490      495
306 Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys
307      500      505      510
308 Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp

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